

1 GAATATGATG ACCCTAATGC AACAAATATCT AACATACTAT CCGAGCTTCG  
51 GTCATTTGGA AGAACTGCAG ATTTTCCTCC TTCAAAATTA AAGTCAGGTT  
101 ATGGAGAACA TGTATGCTAT GTTCTTGATT GCTTCGCTGA AGAAGCATTG  
151 AAATATATTG GTTTCACCTG GAAAAGGCCA ATATACCCAG TAGAAGAATT  
201 AGAAGAAGAA AGCGTTGCAG AAGATGATGC AGAATTAACA TTAAATAAAG  
251 TGGATGAAGA ATTTGTGGAA GAAGAGACAG ATAATGAAGA AAACTTTATT  
301 GATCTCAACG TTTTAAAGGC CCAGACATAT CACTTGGATA TGAACGAGAC  
351 TGCCAAACAA GAAGATATTT TGAATCCAC AACAGATGCT GCAGAATGGA  
401 GCCTAGAAGT GGAACGTGTA CTACCGCAAC TGAAAGTCAC GATTAGGACT  
451 GACAATAAGG ATTGGAGAAT CCATGTTGAC CAAATGCACC AGCACAGAAG  
501 TGGAATTGAA TCTGCTCTAA AGGAGACCAA GGGATTTTTG GACAACTCC  
551 ATAATGAAAT TACTAGGACT TTGGAAAAGA TCAGCAGCCG AGAAAAGTAC  
601 ATCAACAATC AGCCGGGAGC CCATGGAGCA CTGTCCTCAG AGATGCGCAG  
651 GTTAGGCTCA CTGTCTAGGC CAGGCCACC TTAGTCACTG TGGACTGGCA  
701 ATGGAAGCTC TTCCTGGACA CACCTGCCCT AGCCCTCACC CTGGGGTGGA  
751 AGAGAAATGA GCTTGGCTTG CAACTCAGAC CATTCCACGG AGGCATCCTC  
801 CCCTTCCCTG GGCTGGTGAA TAAAAGTTTC CTGAGGTCAA GGACTTCCTT  
851 TTCCCTGCCA AAATGGTGTC CAGAACTTTG AGGCCAGAGG TGATCCAGTG

FIG.1A

901 ATTTGGGAGC TGCAGGTCAC ACAGGCTGCT CAGAGGGCTG CTGAACAGGA  
951 TGTCTCGGA CGACAGGCAC CTGGGCTCCA GCTGCGGCTC CTTTCATCAAG  
1001 ACTGAGCCGT CCAGCCCGTC CTCGGGCATA GATGCCCTCA GCCACCACAG  
1051 CCCCAGTGGC TCGTCCGACG CCAGCGGCGG CTTTGGCCTG GCCCTGGGCA  
1101 CCCACGCCAA CGGTCTGGAC TCGCCACCCA TGTTTGCAGG CGCCGGGCTG  
1151 GGAGGCACCC CATGCCGCAA GAGCTACGAG GACTGTGCCA GCGGCATCAT  
1201 GGAGGACTCG GCCATCAAGT GCGAGTACAT GCTCAACGCC ATCCCCAAGC  
1251 GCCTGTGCCT CGTGTGCGGG GACATTGCCT CTGGCTACCA CTACGGCGTG  
1301 GCCTCCTGCG AGGCTTGCAA GGCCTTCTTC AAGAGGACTA TCCAAGGGAA  
1351 CATTGAGTAC AGCTGCCCCG CCACCAACGA GTGCGAGATC ACCAAACGGA  
1401 GGCGCAAGTC CTGCCAGGCC TGCCGCTTCA TGAAATGCCT CAAAGTGGGG  
1451 ATGCTGAAGG AAGGTGTGCG CCTTGATCGA GTGCGTGGAG GCCGTCAGAA  
1501 ATACAAGCGA CGGCTGGACT CAGAGAGCAG CCCATACCTG AGCTTACAAA  
1551 TTTCTCCACC TGCTAAAAAG CCATTGACCA AGATTGTCTC ATACCTACTG  
1601 GTGGCTGAGC CGGACAAGCT CTATGCCATG CCTCCCCCTG GTATGCCTGA  
1651 GGGGGACATC AAGGCCCTGA CCACTCTCTG TGACCTGGCA GACCGAGAGC  
1701 TTGTGGTCAT CATTGGCTGG GCCAAGCACA TCCCAGGCTT CTCAAGCCTC  
1751 TCCCTGGGGG ACCAGATGAG CCTGCTGCAG AGTGCCTGGA TGGAAATCCT

FIG.1B

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1801 CATCCTGGGC ATCGTGTACC GCTCGCTGCC CTACGACGAC AAGCTGGTGT  
1851 ACGCTGAGGA CTACATCATG GATGAGGAGC ACTCCCGCCT CGCGGGGCTG  
1901 CTGGAGCTCT ACCGGGCCAT CCTGCAGCTG GTACGCAGGT ACAAGAAGCT  
1951 CAAGGTGGAG AAGGAGGAGT TTGTGACGCT CAAGGCCCTG GCCCTCGCCA  
2001 ACTCCGATTC CATGTACATC GAGGATCTAG AGGCTGTCCA GAAGCTGCAG  
2051 GACCTGCTGC ACGAGGCACT GCAGGACTAC GAGCTGAGCC AGCGCCATGA  
2101 GGAGCCCTGG AGGACGGGCA AGCTGCTGCT GACACTGCCG CTGCTGCGGC  
2151 AGACGGCCGC CAAGGCCGTG CAGCACTTCT ATAGCGTCAA ACTGCAGGGC  
2201 AAAGTGCCCA TGCACAACT CTCCTGGAG ATGCTGGAGG CCAAGGCCTG  
2251 GGCCAGGGCT GACTCCCTTC AGGAGTGGAG GCCACTGGAG CAAGTGCCCT  
2301 CTCCCCTCCA CCGAGCCACC AAGAGGCAGC ATGTGCATTT CCTAACTCCC  
2351 TTGCCCCCTC CCCCATCTGT GGCCTGGGTG GGCCTGCTC AGGCTGGATA  
2401 CCACCTGGAG GTTTTCCTTC CGCAGAGGGC AGGTTGGCCA AGAGCAGCTT  
2451 AGAGGATCTC CCAAGGATGA AAGAATGTCA AGCCATGATG GAAAATGCCC  
2501 CTTCCAATCA GCTGCCTTCA CAAGCAGGGA TCAGAGCAAC TCCCCGGGGA  
2551 TCCCCAATCC ACGCCCTTCT AGTCCAACCC CCCTCAATGA GAGAGGCAGG  
2601 CAGATCTCAC CCAGCACTAG GACACCAGGA GGCCAGGGAA AGCATCTCTG  
2651 GCTCACCATG TAACATCTGG CTTGGAGCAA GTGGGTGTTC TGCACACCAG  
2701 GCAGCTGCAC CTCCTGGAT CTAGTGTTC TGCGAGTGAC CTCCTTCAG  
2751 AGCCCCTCTA GCAGAGTGGG GCGGAAGTCC TGATGGTTGG TGTCCATGAG  
2801 GTGGAAG (SEQ.ID NO:1)

FIG.1C

1005494.041602

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GAATATGATGACCCTAATGCAACAATATCTAACATACTATCCGAGCTTCGGTCATTTGGA  
1 -----+-----+-----+-----+-----+-----+ 60  
CTTATACTACTGGGATTACGTTGTTATAGATTGTATGATAGGCTCGAAGCCAGTAAACCT

AGAACTGCAGATTTTCCTCCTTCAAAATTAAAGTCAGGTTATGGAGAACATGTATGCTAT  
61 -----+-----+-----+-----+-----+-----+ 120  
TCTTGACGTCTAAAAGGAGGAAGTTTAAATTCAGTCCAATACCTCTTGTACATACGATA

GTTCTTGATTGCTTCGCTGAAGAAGCATTGAAATATATTGGTTTCACCTGGAAAAGGCCA  
121 -----+-----+-----+-----+-----+-----+ 180  
CAAGAACTAACGAAGCGACTTCTTCGTAACTTTATATAACCAAAGTGGACCTTTTCCGGT

ATATACCCAGTAGAAGAATTAGAAGAAGAAAGCGTTGCAGAAGATGATGCAGAATTAACA  
181 -----+-----+-----+-----+-----+-----+ 240  
TATATGGGTCATCTTCTTAATCTTCTTCTTCGCAACGTCTTCTACTACGTCTTAATTGT

TTAAATAAAGTGGATGAAGAATTTGTGGAAGAAGAGACAGATAATGAAGAAAACCTTTATT  
241 -----+-----+-----+-----+-----+-----+ 300  
AATTTATTTACCTACTTCTTAACACCTTCTTCTGTCTATTACTTCTTTTGAATAA

GATCTCAACGTTTTAAAGGCCAGACATATCACTTGGATATGAACGAGACTGCCAAACAA  
301 -----+-----+-----+-----+-----+-----+ 360  
CTAGAGTTGCAAAATTTCCGGGTCTGTATAGTGAACCTATACTTGCTCTGACGGTTTGT

GAAGATATTTTGAATCCACAACAGATGCTGCAGAATGGAGCCTAGAAGTGAACGTGTA  
361 -----+-----+-----+-----+-----+-----+ 420  
CTTCTATAAAACCTTAGGTGTTGTCTACGACGTCTTACCTCGGATCTTACCTTGACAT

CTACCGCAACTGAAAGTCACGATTAGGACTGACAATAAGGATTGGAGAATCCATGTTGAC  
421 -----+-----+-----+-----+-----+-----+ 480  
GATGGCGTTGACTTTAGTGCTAATCCTGACTGTTATTCCTAACCTCTTAGGTACAACCTG

CAAATGCACCAGCACAGAAGTGAATTGAATCTGCTCTAAAGGAGACCAAGGGATTTTTG  
481 -----+-----+-----+-----+-----+-----+ 540  
GTTTACGTGGTCGTGCTTACCTTAACCTTAGACGAGATTTCTCTGGTTCCCTAAAAAC

FIG.2A

10054941.041600

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541 GACAAACTCCATAATGAAATTACTAGGACTTTGGAAAAGATCAGCAGCCGAGAAAAGTAC 600  
-----+-----+-----+-----+-----+-----+  
CTGTTTGAGGTATTACTTTAATGATCCTGAAACCTTTTCTAGTCGTCGGCTCTTTTCATG

601 ATCAACAATCAGCCGGGAGCCCATGGAGCACTGTCCTCAGAGATGCGCAGGTTAGGCTCA 660  
-----+-----+-----+-----+-----+-----+  
TAGTTGTTAGTCGGCCCTCGGGTACCTCGTGACAGGAGTCTCTACGCGTCCAATCCGAGT

661 CTGTCTAGGCCAGGCCACCTTAGTCACTGTGGACTGGCAATGGAAGCTCTTCCTGGACA 720  
-----+-----+-----+-----+-----+-----+  
GACAGATCCGGTCCGGGTGGAATCAGTGACACCTGACCGTTACCTTCGAGAAGGACCTGT

721 CACCTGCCCTAGCCCTCACCTGGGGTGAAGAGAAATGAGCTTGGCTTGCAACTCAGAC 780  
-----+-----+-----+-----+-----+-----+  
GTGGACGGGATCGGGAGTGGGACCCACCTTCTCTTTACTCGAACCGAACGTTGAGTCTG

781 CATTCCACGGAGGCATCCTCCCCTTCCCTGGGCTGGTGAATAAAAGTTTCCTGAGGTCAA 840  
-----+-----+-----+-----+-----+-----+  
GTAAGGTGCCTCCGTAGGAGGGGAAGGGACCCGACCACTTATTTTCAAAGGACTCCAGTT

841 GGACTTCCTTTTCCCTGCCAAATGGTGTCCAGAACTTTGAGGCCAGAGGTGATCCAGTG 900  
-----+-----+-----+-----+-----+-----+  
CCTGAAGGAAAAGGGACGGTTTTACCACAGGTCTTGAAACTCCGGTCTCCACTAGGTCAC

901 ATTTGGGAGCTGCAGGTACACAGGCTGCTCAGAGGGCTGCTGAACAGGATGTCCTCGGA 960  
-----+-----+-----+-----+-----+-----+  
TAAACCCTCGACGTCCAGTGTGTCCGACGAGTCTCCCGACGACTTGTCCTACAGGAGCCT  
M S S D

961 CGACAGGCACCTGGGCTCCAGCTGCGGCTCCTTCATCAAGACTGAGCCGTCCAGCCCCTC 1020  
-----+-----+-----+-----+-----+-----+  
GCTGTCCGTGGACCCGAGGTGCACGCCGAGGAAGTAGTTCTGACTCGGCAGGTGCGGCAG  
D R H L G S S C G S F I K T E P S S P S

FIG.2B

20054941.04.1602

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CTCGGGCATAGATGCCCTCAGCCACCACAGCCCCAGTGGCTCGTCCGACGCCAGCGGCGG  
1021 -----+-----+-----+-----+-----+-----+ 1080  
GAGCCCGTATCTACGGGAGTCCGTGGTGTCTGGGGTCACCGAGCAGGCTGCGGTGCGCGCC  
S G I D A L S H H S P S G S S D A S G G

CTTTGGCCTGGCCCTGGGCACCCACGCCAACGGTCTGGACTCGCCACCCATGTTTGCAGG  
1081 -----+-----+-----+-----+-----+-----+ 1140  
GAAACCGGACCGGGACCCGTGGGTGCGGTTGCCAGACCTGAGCGGTGGGTACAAACGTCC  
F G L A L G T H A N G L D S P P M F A G

CGCCGGGCTGGGAGGCACCCCATGCCGCAAGAGCTACGAGGACTGTGCCAGCGGCATCAT  
1141 -----+-----+-----+-----+-----+-----+ 1200  
GCGGCCCCGACCCTCCGTGGGGTACGGCGTTCTCGATGCTCCTGACACGGTCGCCGTAGTA  
A G L G G T P C R K S Y E D C A S G I M

GGAGGACTCGGCCATCAAGTGCGAGTACATGCTCAACGCCATCCCCAAGCGCCTGTGCCT  
1201 -----+-----+-----+-----+-----+-----+ 1260  
CCTCCTGAGCCGGTAGTTACGCTCATGTACGAGTTGCGGTAGGGGTTGCGGGACACGGA  
E D S A I K C E Y M L N A I P K R L C L

CGTGTGCGGGGACATTGCCTCTGGCTACCACTACGGCGTGGCCTCCTGCGAGGCTTGCAA  
1261 -----+-----+-----+-----+-----+-----+ 1320  
GCACACGCCCCTGTAACGGAGACCGATGGTGATGCCGCACCGGAGGACGCTCCGAACGTT  
V C G D I A S G Y H Y G V A S C E A C K

GGCCTTCTTCAAGAGGACTATCCAAGGGAACATTGAGTACAGCTGCCCCGGCCACCAACGA  
1321 -----+-----+-----+-----+-----+-----+ 1380  
CCGGAAGAAGTTCTCCTGATCGGTTCCCTTGTAACCTCATGTCGACGGGCCGGTGGTTGCT  
A F F K R T I Q G N I E Y S C P A T N E

GTGCGAGATCACCAAACGGAGGCGCAAGTCCTGCCAGGCCTGCCGCTTCATGAAATGCCT  
1381 -----+-----+-----+-----+-----+-----+ 1440  
CACGCTCTAGTGGTTTGCCTCCGCGTTCAGGACGGTCCGGACGGCGAAGTACTTTACGGA  
C E I T K R R R K S C Q A C R F M K C L

FIG.2C

1005494.04303

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CAAAGTGGGGATGCTGAAGGAAGGTGTGCGCCTTGATCGAGTGCGTGGAGGCCGTCAGAA  
1441 -----+-----+-----+-----+-----+-----+ 1500  
GTTTCACCCCTACGACTTCCTTCCACACGCGGAAGCTAGCTCACGCACCTCCGGCAGTCTT  
K V G M L K E G V R L D R V R G G R Q K

ATACAAGCGACGGCTGGACTCAGAGAGCAGCCATACCTGAGCTTACAAATTTCTCCACC  
1501 -----+-----+-----+-----+-----+-----+ 1560  
TATGTTGCGTGCCGACCTGAGTCTCTCGTCGGGTATGGACTCGAATGTTTAAAGAGGTGG  
Y K R R L D S E S S P Y L S L Q I S P P

TGCTAAAAAGCCATTGACCAAGATTGTCTCATACCTACTGGTGGCTGAGCCGGACAAGCT  
1561 -----+-----+-----+-----+-----+-----+ 1620  
ACGATTTTTTCGGTAACTGGTTCTAACAGAGTATGGATGACCACCGACTCGGCCTGTTTGA  
A K K P L T K I V S Y L L V A E P D K L

CTATGCCATGCCTCCCCCTGGTATGCCTGAGGGGGACATCAAGGCCCTGACCACTCTCTG  
1621 -----+-----+-----+-----+-----+-----+ 1680  
GATACGGTACGGAGGGGGACCATACGGACTCCCCCTGTAGTTCCGGGACTGGTGAGAGAC  
Y A M P P P G M P E G D I K A L T T L C

TGACCTGGCAGACCGAGAGCTTGTGGTCATCATTGGCTGGGCCAAGCACATCCCAGGCTT  
1681 -----+-----+-----+-----+-----+-----+ 1740  
ACTGGACCGTCTGGCTCTCGAACACCAAGTAGTAACCGACCCGGTTCGTGTAGGGTCCGAA  
D L A D R E L V V I I G W A K H I P G F

CTCAAGCCTCTCCCTGGGGGACCAGATGAGCCTGCTGCAGAGTGCCTGGATGGAAATCCT  
1741 -----+-----+-----+-----+-----+-----+ 1800  
GAGTTCGGAGAGGGACCCCTGGTCTACTCGGACGACGTCTCACGGACCTACCTTTAGGA  
S S L S L G D Q M S L L Q S A W M E I L

CATCCTGGGCATCGTGTACCGCTCGCTGCCCTACGACGACAAGCTGGTGTACGCTGAGGA  
1801 -----+-----+-----+-----+-----+-----+ 1860  
GTAGGACCCGTAGCACATGGCGAGCGACGGGATGCTGCTGTTTCGACCACATGCGACTCCT  
I L G I V Y R S L P Y D D K L V Y A E D

FIG.2D

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CTACATCATGGATGAGGAGCACTCCCGCCTCGCGGGGCTGCTGGAGCTCTACCGGGCCAT  
 1861 -----+-----+-----+-----+-----+-----+ 1920  
 GATGTAGTACCTACTCCTCGTGAGGGCGGAGCGCCCCGACGACCTCGAGATGGCCCCGTA  
 Y I M D E E H S R L A G L L E L Y R A I

CCTGCAGCTGGTACGCAGGTACAAGAAGCTCAAGGTGGAGAAGGAGGAGTTTGTGACGCT  
 1921 -----+-----+-----+-----+-----+-----+ 1980  
 GGACGTCGACCATGCGTCCATGTTCTTCGAGTTCCACCTCTTCCTCCTCAAACACTGCGA  
 L Q L V R R Y K K L K V E K E E F V T L

CAAGGCCCTGGCCCTCGCCAACTCCGATTCCATGTACATCGAGGATCTAGAGGCTGTCCA  
 1981 -----+-----+-----+-----+-----+-----+ 2040  
 GTTCCGGGACCGGGAGCGGTTGAGGCTAAGGTACATGTAGCTCCTAGATCTCCGACAGGT  
 K A L A L A N S D S M Y I E D L E A V Q

GAAGCTGCAGGACCTGCTGCACGAGGCACTGCAGGACTACGAGCTGAGCCAGCGCCATGA  
 2041 -----+-----+-----+-----+-----+-----+ 2100  
 CTTTCGACGTCCTGGACGACGTGCTCCGTGACGTCCTGATGCTCGACTCGGTGCGGTACT  
 K L Q D L L H E A L Q D Y E L S Q R H E

GGAGCCCTGGAGGACGGGCAAGCTGCTGCTGACACTGCCGCTGCTGCGGCAGACGGCCGC  
 2101 -----+-----+-----+-----+-----+-----+ 2160  
 CCTCGGGACCTCCTGCCCGTTTCGACGACGACTGTGACGGCGACGACGCCGTCTGCCGGCG  
 E P W R T G K L L L T L P L L R Q T A A

CAAGGCCGTGCAGCACTTCTATAGCGTCAAACCTGCAGGGCAAAGTGCCCATGCACAACT  
 2161 -----+-----+-----+-----+-----+-----+ 2220  
 GTTCCGGCACGTCGTGAAGATATCGCAGTTTGACGTCCCGTTTCACGGGTACGTGTTTGA  
 K A V Q H F Y S V K L Q G K V P M H K L

CTTCCTGGAGATGCTGGAGGCCAAGGCCTGGGCCAGGGCTGACTCCCTTCAGGAGTGGAG  
 2221 -----+-----+-----+-----+-----+-----+ 2280  
 GAAGGACCTCTACGACCTCCGGTTCCGGACCCGGTCCCGACTGAGGGAAGTCCTCACCTC  
 F L E M L E A K A W A R A D S L Q E W R

FIG.2E

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MSSDDRHLGS SCGSFIKTEP SSPSSGIDAL SHHSPSGSSD ASGGFGLALG  
THANGLDSPP MFAGAGLGGT PCRKSYEDCA SGIMEDSAIK CEYMLNAIPK  
RLCLVCGDIA SGYHYGVASC EACKAFFKPT IOGNIYSCP ATNICEITKR  
RRKSCOACRF MKCLKVGMLK EGVRLDRVRG GRQKYKRRLD SESSPYLSLQ  
ISPPAKKPLT KIVSYLLVAE PDKLYAMPPP GMPRGDIKAL TTLCDLADRE  
LVVIIGWAKH IPGFSSLSLG DQMSLLQSAW MEILILGIVY RSLPYDDKLK  
YAEDYIMDEE HSRLAGLLEL YRAILQLVRR YKCLKVEKEE FVTLKALALA  
NSDSMYIEDL EAVQKLQDLL HEALQDYELS QRHEEPWRTG KLLLTLP LLR  
QTAAKAVQHF YSVKLQGKVP MHKLFLEMLE AKAWARADSL QEWRPLEQVP  
SPLHRATKRQ HVHFLTPLPP PPSVAWVGTA QAGYHLEVFL PQRAGWPRAA  
(SEQ ID NO:2)

FIG.3

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1 GCGGGCCGCC AGTGTGGTGG AATTCGGCTT GTCACTAGGA ??????????  
51 GTTAATTGCA CTGTGCTCTG TCAAGGAAAC TTTGATTTAT AGCTGGGGTG  
101 CACAAATAAT GGTGCGCGT CGCACATGGA TTCGGTAGAA CTTTGCCTTC  
151 CTGAATCTTT TTCCCTGCAC TACGAGGAAG AGCTTCTCTG CAGAATGTCA  
201 AACAAAGATC GACACATTGA TTCCAGCTGT TCGTCCTTCA TCAAGACGGA  
251 ACCTTCCAGC CCAGCCTCCC TGACGGACAG CGTCAACCAC CACAGCCCTG  
301 GTGGCTCTTC AGACGCCAGT GGGAGCTACA GTTCAACCAT GAATGGCCAT  
351 CAGAACGGAC TTGACTCGCC ACCTCTCTAC CTTTCTGCTC CTATCCTGGG  
401 AGGTAGTGGG CCTGTCAGGA AACTGTATGA TGA CTGCTCC AGCACCATTG  
451 TTGAAGATCC CCAGACCAAG TGTGAATACA TGCTCAACTC GATGCCCAAG  
501 AGACTGTGTT TAGTGTGTGG TGACATCGCT TCTGGGTACC ACTATGGGGT  
551 AGCATCATGT GAAGCCTGCA AGGCATTCTT CAAGAGGACA ATTCAAGGCA  
601 ATATAGAATA CAGCTGCCCT GCCACGAATG AATGTGAAAT CACAAAGCGC  
651 AGACGTAAAT CCTGCCAGGC TTGCCGCTTC ATGAAGTGTT TAAAAGTGGG  
701 CATGCTGAAA GAAGGGGTGC GTCTTGACAG AGTACGTGGA GGTCGGCAGA  
751 AGTACAAGCG CAGGATAGAT GCGGAGAACA GCCCATACCT GAACCCTCAG  
801 CTGGTTCAGC CAGCCAAAAA GCCATATAAC AAGATTGTCT CACATTTGTT  
851 GGTGGCTGAA CCGGAGAAGA TCTATGCCAT GCCTGACCCT ACTGTCCCCG  
901 ACAGTGACAT CAAAGCCCTC ACTACAGTGT GTGACTTGGC CGACCGAGAG  
951 TTGGTGGTTA TCATTGGATG GGCGAAGCAT ATTCCAGGCT TCTCCACGCT  
1001 GTCCCTGGCG GACCAGATGA GCCTTCTGCA GAGTGCTTGG ATGGAAATTT  
1051 TGATCCTTGG TGTCGTATAC CGGTCTCTTT CATTTGAGGA TGA ACTTGTC

FIG.4A

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1101 TATGCAGACG ATTATATAAT GGACGAAGAC CAGTCCAAAT TAGCAGGCCT  
1151 TCTTGATCTA AATAATGCTA TCCTGCAGCT GGTAAGAGAA TACAAGAGCA  
1201 TGAAGCTGGA AAAAGAAGAA TTTGTCACCC TCAAAGCTAT AGCTCTTGCT  
1251 AATTCAGACT CCATGCACAT AGAAGATGTT GAAGCCGTTT AGAAGCTTCA  
1301 GGATGTCTTA CATGAAGCGC TGCAGGATTA TGAAGCTGGC CAGCACATGG  
1351 AAGACCCTCG TCGAGCTGGC AAGATGCTGA TGACACTGCC ACTCCTGAGG  
1401 CAGACCTCTA CCAAGGCCGT GCAGCATTTT TACAACATCA AACTAGAAGG  
1451 CAAAGTCCCA ATGCACAAAC TTTTTTTGGA AATGTTGGAG GCCAAGGTCT  
1501 GACTAAAAGC TCCCTGGGCC TTCCCATCCT TCATGTTGAA AAAGGGAAAA  
1551 TAAACCCAAG AGTGATGTCG AAGAACTTA GAGTTTAGTT AACAACATCA  
1601 AAAATCAACA GACTGCACTG ATAATTTAGC AGCAAGACTA TGAAGCAGCT  
1651 TTCAGATTCC TCCATAGGTT CCTGATGAGT TCTTTCTACT TTCTCCATCA  
1701 TCTTCTTTCC TCTTTCTTCC CACATTTCTC TTTCTCTTTA TTTTTTCTCC  
1751 TTTTCTTCTT TCACCTCCCT TATTTCTTTG CTTCTTTTCA TCCTAGTTCC  
1801 CATTCTCCTT TATTTTCTTC CCGTCTGCCT GCCTTCTTTC TTTTCTTTAC  
1851 CTA CTCTCAT TCCTCTCTTT TCTCATCCTT CCCCTTTTTT CTAAATTTGA  
1901 AATAGCTTTA GTTTAAAAAA AAAATCCTC CCTTCCCCCT TTCCTTTCCC  
1951 TTTCTTTCTT TTTTCCCTTT CCTTTTCCCT TTCCTTTCTT TTCCTCTTGA  
2001 CCTTCTTTCC ATCTTTCTTT TTCTTCCTTC TGCTGCTGAA CTTTTAAAAG  
2051 AGGTCTCTAA GTGAAGAGAG ATGGAAGCCA GCCCTGCCAA AGGATGGAGA  
2101 TCCATAATAT GGATGCCAGT GAACTTATTG TGAACCATAC CGTCCCCAAT  
2151 GACTAAGGAA TCAAAGAGAG AGAACCAACG TTCCTAAAAG TACAGTGCAA  
2201 CATATACAAA TTGACTGAGT GCAGTATTAG ATTTTCATGGG AGCAGCCTCT

FIG.4B

2251 AATTAGACAA CTTAAGCAAC GTTGCATCGG CTGCTTCTTA TCATTGCTTT  
2301 TCCATCTAGA TCAGTTACAG CCATTTGATT CCTTAATTGT TTTTCAAGT  
2351 CTTCCAGGTA TTTGTTAGTT TAGCTACTAT GTAACTTTTT CAGGGAATAG  
2401 TTTAAGCTTT ATTCATTCAT GCAATACTAA AGAGAAATAA GAATACTGCA  
2451 ATTTTGTGCT GGCTTTGAAC AATTACGAAC AATAATGAAG GACAAATGAA  
2501 TCCTGAAGGA AGATTTTTTAA AAATGTTTTG TTTCTTCTTA CAAATGGAGA  
2551 TTTTTTTGTA CCAGCTTTAC CACTTTTCAG CCATTTATTA ATATGGGAAT  
2601 TTAACCTACT CAAGCAATAG TTGAAGGGAA GGTGCATATT ATCACGGATG  
2651 CAATTTATGT TGTGTGCCAG TCTGGTCCCA AACATCAATT TCTTAACATG  
2701 AGCTCCAGTT TACCTAAATG TTCACTGACA CAAAGGATGA GATTACACCT  
2751 ACAGTGACTC TGAGTAGTCA CATATATAAG CACTGCACAT GAGATATAGA  
2801 TCCGTAGAAT TGTCAGGAGT GCACCTCTCT ACTTGGGAGG TACAATTGCC  
2851 ATATGATTTT TAGCTGCCAT GGTGGTTAGG AATGTGATAC TGCCTGTTTG  
2901 CAAAGTCACA GACCTTGCCT CAGAAGGAGC TGTGAGCCAG TATTCATTTA  
2951 AGAGAATTCC ACCACACTGG CGGCCCGCGC TTGAT (SEQ ID NO:3)

FIG.4C

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1 GCGGGCCGCCAGTGTGGTGGAAATTCGGCTTGCTACTAGGAGAACATTTGTGTTAATTGCA 60  
 -----+-----+-----+-----+-----+-----+  
 CGCCCGGCGGTACACCACCTTAAGCCGAACAGTGATCCTCTTGTAACACAATTAACGT

61 CTGTGCTCTGTCAAGGAACTTTGATTTATAGCTGGGGTGCACAAATAATGGTTGCCGGT 120  
 -----+-----+-----+-----+-----+-----+  
 GACACGAGACAGTTCCTTTGAACTAAATATCGACCCACGTGTTTATTACCAACGGCCA

121 CGCACATGGATTCCGGTAGAACTTTGCCTTCCTGAATCTTTTTCCCTGCACTACGAGGAAG 180  
 -----+-----+-----+-----+-----+-----+  
 GCGTGTAACCTAAGCCATCTTGAAACGGAAGGACTTAGAAAAAGGGACGTGATGCTCCTTC  
 M D S V E L C L P E S F S L H Y E E E

181 AGCTTCTCTGCAGAATGTCAAACAAAGATCGACACATTGATTCCAGCTGTTTCGTCCTTCA 240  
 -----+-----+-----+-----+-----+-----+  
 TCGAAGAGACGTCTTACAGTTTGTTTCTAGCTGTGTAACCTAAGGTCGACAAGCAGGAAGT  
 L L C R M S N K D R H I D S S C S S F I

241 TCAAGACGGAACCTTCCAGCCCAGCCTCCCTGACGGACAGCGTCAACCACCACAGCCCTG 300  
 -----+-----+-----+-----+-----+-----+  
 AGTTCTGCCTTGGAAGGTGCGGTGCGGAGGACTGCCTGTGCGAGTTGGTGGTGTGCGGGAC  
 K T E P S S P A S L T D S V N H H S P G

301 GTGGCTCTTCAGACGCCAGTGGGAGCTACAGTTCAACCATGAATGGCCATCAGAACGGAC 360  
 -----+-----+-----+-----+-----+-----+  
 CACCGAGAAGTCTGCGGTACCCCTCGATGTCAAGTTGGTACTTACCGGTAGTCTTGCCTG  
 G S S D A S G S Y S S T M N G H Q N G L

361 TTGACTCGCCACCTCTCTACCCTTCTGCTCCTATCCTGGGAGGTAGTGGGCCTGTCAGGA 420  
 -----+-----+-----+-----+-----+-----+  
 AACTGAGCGGTGGAGAGATGGGAAGACGAGGATAGGACCCTCCATCACCCGGACAGTCCT  
 D S P P L Y P S A P I L G G S G P V R K

FIG.5A

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421 AACTGTATGATGACTGCTCCAGCACCATTGTTGAAGATCCCCAGACCAAGTGTGAATACA 480  
 -----+-----+-----+-----+-----+  
 TTGACATACTACTGACGAGGTCGTGGTAACAATTCTAGGGGTCTGGTTCACACTTATGT  
 L Y D D C S S T I V E D P Q T K C E Y M

481 TGCTCAACTCGATGCCCAAGAGACTGTGTTTAGTGTGTGGTGACATCGCTTCTGGGTACC 540  
 -----+-----+-----+-----+-----+  
 ACGAGTTGAGCTACGGGTTCTCTGACACAAATCACACACCACTGTAGCGAAGACCCATGG  
 L N S M P K R L C L V C G D I A S G Y H

541 ACTATGGGGTAGCATCATGTGAAGCCTGCAAGGCATTCTTCAAGAGGACAATTCAAGGCA 600  
 -----+-----+-----+-----+-----+  
 TGATACCCCATCGTAGTACACTTCGGACGTTCCGTAAGAAGTTCTCCTGTTAAGTTCGGT  
Y G V A S C E A C K A F F K R T I Q G N

601 ATATAGAATACAGCTGCCCTGCCACGAATGAATGTGAAATCACAAAGCGCAGACGTAAAT 660  
 -----+-----+-----+-----+-----+  
 TATATCTTATGTCGACGGGACGGTGCTTACTTACACTTTAGTGTTCGCGTCTGCATTTA  
I E Y S C P A T N E C E I T K R R R K S

661 CCTGCCAGGCTTGCCGCTTCATGAAGTGTTTAAAGTGGGCATGCTGAAAGAAGGGGTGC 720  
 -----+-----+-----+-----+-----+  
 GGACGGTCCGAACGGCGAAGTACTTCACAAATTTTCACCCGTACGACTTTCTTCCCCACG  
C Q A C R F M K C L K V G M L K E G V R

721 GTCTTGACAGAGTACGTGGAGGTCGGCAGAAGTACAAGCGCAGGATAGATGCGGAGAACA 780  
 -----+-----+-----+-----+-----+  
 CAGAACTGTCTCATGCACCTCCAGCCGTCTTCATGTTGCGGTCCTATCTACGCCTCTTGT  
 L D R V R G G R Q K Y K R R I D A E N S

781 GCCCATACCTGAACCCTCAGCTGGTTCAGCCAGCCAAAAAGCCATATAACAAGATTGTCT 840  
 -----+-----+-----+-----+-----+  
 CGGGTATGGACTTGGGAGTCGACCAAGTCGGTCGGTTTTTCGGTATATTGTTCTAACAGA  
 P Y L N P Q L V Q P A K K P Y N K I V S

FIG.5B

20254941.04.602

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841 CACATTTGTTGGTGGCTGAACCGGAGAAGATCTATGCCATGCCTGACCCTACTGTCCCCG 900  
 -----+-----+-----+-----+-----+-----+  
 GTGTAAACAACCAACCGACTTGGCCTCTTCTAGATACGGTACGGACTGGGATGACAGGGGC  
 H L L V A E P E K I Y A M P D P T V P D  
  
 901 ACAGTGACATCAAAGCCCTCACTACACTGTGTGACTTGGCCGACCGAGAGTTGGTGGTTA 960  
 -----+-----+-----+-----+-----+-----+  
 TGTCAGTGTAGTTTTCGGGAGTGATGTGACACACTGAACCGGCTGGCTCTCAACCACCAAT  
 S D I K A L T T L C D L A D R E L V V I  
  
 961 TCATTGGATGGGCGAAGCATATTCCAGGCTTCTCCACGCTGTCCCTGGCGGACCAGATGA 1020  
 -----+-----+-----+-----+-----+-----+  
 AGTAACCTACCCGCTTCGTATAAGGTCCGAAGAGGTGCGACAGGGACCGCCTGGTCTACT  
 I G W A K H I P G F S T L S L A D Q M S  
  
 1021 GCCTTCTGCAGAGTGCTTGGATGGAAATTTTGATCCTTGGTGTCTGATACCGGTCTCTTT 1080  
 -----+-----+-----+-----+-----+-----+  
 CGGAAGACGTCTCACGAACCTACCTTTAAACTAGGAACACAGCATATGGCCAGAGAAA  
 L L Q S A W M E I L I L G V V Y R S L S  
  
 1081 CATTTGAGGATGAACTTGTCTATGCAGACGATTATATAATGGACGAAGACCAGTCCAAAT 1140  
 -----+-----+-----+-----+-----+-----+  
 GTAAACTCCTACTTGAACAGATACGTCTGCTAATATATTACCTGCTTCTGGTCAGGTTTA  
 F E D E L V Y A D D Y I M D E D Q S K L  
  
 1141 TAGCAGGCCTTCTTGATCTAAATAATGCTATCCTGCAGCTGGTAAAGAAATACAAGAGCA 1200  
 -----+-----+-----+-----+-----+-----+  
 ATCGTCCGGAAGAACTAGATTTATTACGATAGGACGTCGACCATTTCTTTATGTTCTCGT  
 A G L L D L N N A I L Q L V K K Y K S M  
  
 1201 TGAAGCTGGAAAAAGAAGAATTTGTCACCCTCAAAGCTATAGCTCTTGCTAATTCAGACT 1260  
 -----+-----+-----+-----+-----+-----+  
 ACTTCGACCTTTTTCTTCTTAAACAGTGGGAGTTTCGATATCGAGAACGATTAAGTCTGA  
 K L E K E E F V T L K A I A L A N S D S

FIG.5C



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1261 CCATGCACATAGAAGATGTTGAAGCCGTTTCAGAAGCTTCAGGATGTCTTACATGAAGCGC 1320  
 -----+-----+-----+-----+-----+-----+  
 GGTACGTGTATCTTCTACAACCTTCGGCAAGTCTTCGAAGTCCTACAGAATGTACTTCGCG  
 M H I E D V E A V Q K L Q D V L H E A L

1321 TGCAGGATTATGAAGCTGGCCAGCACATGGAAGACCCTCGTCGAGCTGGCAAGATGCTGA 1380  
 -----+-----+-----+-----+-----+-----+  
 ACGTCCTAATACTTCGACCGGTCTGTACCTTCTGGGAGCAGCTCGACCGTTCTACGACT  
 Q D Y E A G Q H M E D P R R A G K M L M

1381 TGACACTGCCACTCCTGAGGCAGACCTCTACCAAGGCCGTGCAGCATTTCTACAACATCA 1440  
 -----+-----+-----+-----+-----+-----+  
 ACTGTGACGGTGAGGACTCCGTCTGGAGATGGTTCCGGCACGTCGTAAAGATGTTGTAGT  
 T L P L L R Q T S T K A V Q H F Y N I K

1441 AACTAGAAGGCAAAGTCCCAATGCACAACTTTTTTTGGAAATGTTGGAGGCCAAGGTCT 1500  
 -----+-----+-----+-----+-----+-----+  
 TTGATCTTCCGTTTCAGGGTTACGTGTTTGAAAAAACCTTTACAACCTCCGGTTCCAGA  
 L E G K V P M H K L F L E M L E A K V \*  
 (SEQ NO ID:4)

1501 GACTAAAAGCTCCCTGGGCCTTCCCATCCTTCATGTTGAAAAAGGGAAAATAAACCCAAG 1560  
 -----+-----+-----+-----+-----+-----+  
 CTGATTTTCGAGGGACCCGGAAGGGTAGGAAGTACAACCTTTTCCCTTTTATTTGGGTTC

1561 AGTGATGTGAAGAACTTAGAGTTTAGTTAACAACATCAAAAATCAACAGACTGCACTG 1620  
 -----+-----+-----+-----+-----+-----+  
 TCACTACAGCTTCTTTGAATCTCAAATCAATTGTTGTAGTTTTTAGTTGTCTGACGTGAC

1621 ATAATTTAGCAGCAAGACTATGAAGCAGCTTTCAGATTCCTCCATAGGTTTCCTGATGAGT 1680  
 -----+-----+-----+-----+-----+-----+  
 TATTAAATCGTCGTTCTGATACTTCGTCGAAAGTCTAAGGAGGTATCCAAGGACTACTCA

FIG.5D

1005494.041602

10054841.041602

1681 TCTTTCTACTTTCTCCATCATCTTCTTTCTCTTTCTTCCCACATTTCTCTTTCTCTTTA 1740  
-----+-----+-----+-----+-----+-----+  
AGAAAGATGAAAGAGGTAGTAGAAGAAAGGAGAAAGAAGGGTGTAAAGAGAAAGAGAAAT

1741 TTTTTCTCCTTTTCTTCTTTTACCTCCCTTATTTCTTTGCTTCTTTCATTCTAGTTCC 1800  
-----+-----+-----+-----+-----+-----+  
AAAAAGAGGAAAAGAAGAAAGTGGAGGGAATAAAGAAACGAAGAAAGTAAGGATCAAGG

1801 CATTCTCCTTTATTTTCTTCCCGTCTGCCTGCCTTCTTTCTTTTCTTTACCTACTCTCAT 1860  
-----+-----+-----+-----+-----+-----+  
GTAAGAGGAAATAAAAGAAGGGCAGACGGACGGAAGAAAGAAAAGAAATGGATGAGAGTA

1861 TCCTCTCTTTTCTCATCCTTCCCTTTTTTCTAAATTTGAAATAGCTTTAGTTTAAAAAA 1920  
-----+-----+-----+-----+-----+-----+  
AGGAGAGAAAAGAGTAGGAAGGGGAAAAAGATTTAACTTTATCGAAATCAAATTTTTT

1921 AAAATCCTCCCTTCCCCCTTTCCCTTTCCCTTCTTTCCTTTTTCCCTTTCCTTTTCCCT 1980  
-----+-----+-----+-----+-----+-----+  
TTTTTAGGAGGGAAGGGGGAAAGGAAAGGGAAAGAAAGGAAAAAGGGAAGGAAAAGGGA

1981 TTCCTTTCCTTTCCTCTTGACCTTCTTCCATCTTCTTTTTCTTCTTCTGCTGCTGAA 2040  
-----+-----+-----+-----+-----+-----+  
AAGGAAAGGAAAGGAGAACTGGAAGAAAGGTAGAAAGAAAAAGAAGGAAGACGACGACTT

FIG.5E

CTTTTAAAAGAGGTCTCTAACTGAAGAGAGATGGAAGCCAGCCCTGCCAAAGGATGGAGA  
2041 -----+-----+-----+-----+-----+ 2100  
GAAAATTTTCTCCAGAGATTGACTTCTCTCTACCTTCGGTCGGGACGGTTTCCTACCTCT

TCCATAATATGGATGCCAGTGAAC TTATTGTGAACCATACCGTCCCCAATGACTAAGGAA  
2101 -----+-----+-----+-----+-----+ 2160  
AGGTATTATACCTACGGTCACTTGAATAACACTTGGTATGGCAGGGTTACTGATTCCTT

TCAAAGAGAGAGAAACCAACGTTCTTAAAAGTACAGTGCAACATATACAAATTGACTGAGT  
2161 -----+-----+-----+-----+-----+ 2220  
AGTTTCTCTCTCTTGGTTGCAAGGATTTTCATGTCACGTTGTATATGTTTAACTGACTCA

GCAGTATTAGATTTTCATGGGAGCAGCCTCTAATTAGACAACCTTAAGCAACGTTGCATCGG  
2221 -----+-----+-----+-----+-----+ 2280  
CGTCATAATCTAAAGTACCCTCGTCGGAGATTAATCTGTTGAATTCGTTGCAACGTAGCC

CTGCTTCTTATCATTGCTTTTCCATCTAGATCAGTTACAGCCATTTGATTCCTTAATTGT  
2281 -----+-----+-----+-----+-----+ 2340  
GACGAAGAATAGTAACGAAAAGGTAGATCTAGTCAATGTCGGTAACTAAGGAATTAACA

FIG.5F

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2341 TTTTCAAGTCTTCCAGGTATTTGTTAGTTTAGCTACTATGTAACTTTTTCAGGGAATAG 2400  
 -----+-----+-----+-----+-----+-----+  
 AAAAAGTTCAGAAGGTCCATAACAATCAAATCGATGATACATTGAAAAAGTCCCTTATC  
  
 2401 TTTAAGCTTTATTCATTCATGCAATACTAAAGAGAAATAAGAATACTGCAATTTTGTGCT 2460  
 -----+-----+-----+-----+-----+-----+  
 AAATTCGAAATAAGTAAGTACGTTATGATTTCTCTTTATTCTTATGACGTTAAACACGA  
  
 2461 GGCTTTGAACAATTACGAACAATAATGAAGGACAAATGAATCCTGAAGGAAGATTTTAA 2520  
 -----+-----+-----+-----+-----+-----+  
 CCGAAACTTGTTAATGCTTGTTATTACTTCCTGTTTACTTAGGACTTCCTTCTAAAAATT  
  
 2521 AAATGTTTTGTTTCTTCTTACAAATGGAGATTTTTTTGTACCAGCTTTACCACTTTTCAG 2580  
 -----+-----+-----+-----+-----+-----+  
 TTTACAAAACAAAGAAGAATGTTTACCTCTAAAAAAACATGGTCGAAATGGTGAAAAGTC  
  
 2581 CCATTTATTAATATGGGAATTTAACTTACTCAAGCAATAGTTGAAGGGAAGGTGCATATT 2640  
 -----+-----+-----+-----+-----+-----+  
 GGTAATAATTATACCCTTAAATTGAATGAGTTCGTTATCAACTTCCCTTCCACGTATAA  
  
 2641 ATCACGGATGCAATTTATGTTGTGTGCCAGTCTGGTCCCAAACATCAATTTCTTAACATG 2700  
 -----+-----+-----+-----+-----+-----+  
 TAGTGCCTACGTTAAATACAACACACGGTCAGACCAGGTTTGTAGTTAAAGAATTGTAC  
  
 2701 AGCTCCAGTTTACCTAAATGTTCACTGACACAAAGGATGAGATTACACCTACAGTGA CTC 2760  
 -----+-----+-----+-----+-----+-----+  
 TCGAGGTCAAATGGATTTACAAGTGA CTGTGTTTCTACTCTAATGTGGATGTGCCTGAG

FIG.5G

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2761 TGAGTAGTCACATATATAAGCACTGCACATGAGATATAGATCCGTAGAATTGTCAGGAGT  
-----+-----+-----+-----+-----+-----+ 2820  
ACTCATCAGTGTATATATTCGTGACGTGTACTCTATATCTAGGCATCTTAACAGTCCTCA

2821 GCACCTCTCTACTTGGGAGGTACAATTGCCATATGATTTCTAGCTGCCATGGTGGTTAGG  
-----+-----+-----+-----+-----+-----+ 2880  
CGTGGAGAGATGAACCCTCCATGTTAACGGTATACTAAAGATCGACGGTACCACCAATCC

2881 AATGTGATACTGCCTGTTTGCAAAGTCACAGACCTTGCCTCAGAAGGAGCTGTGAGCCAG  
-----+-----+-----+-----+-----+-----+ 2940  
TTACACTATGACGGACAAACGTTTCAGTGTCTGGAACGGAGTCTTCCTCGACACTCGGTC

2941 TATTCATTTAAGAGAATTCCACCACACTGGCGGCCCGCGCTTGAT (SEQ ID NO:3)  
-----+-----+-----+-----+-----+ 2985  
ATAAGTAAATTCTCTTAAGGTGGTGTGACCGCCGGGCGCGAACTA (SEQ ID NO:30)

FIG.5H

2025-04-16 14:54:50

1 MDSVELCLPE SFSLHYEEEL LCRMSNKDRH IDSSCSSFIK TEPSSPASLT  
51 DSVNHHSPGG SSDASGSYSS TMNGHQGLD SPPLYPAPI LGGSGPVRKL  
101 YDDCSSTIVE DPQTKCEYML NSMPKRL CLV CGDIASGYHY GVASCEACKA  
151 FFKPTIQGNI EYSCPATNEC EITKRRRKSC QACRFMKCLK VGMLKEGVRL  
201 DRVRGGRQKY KRRIDAENSP YLNPQLVQPA KKPYNKIVSH LLVAEPEKIY  
251 AMPDPTVPDS DIKALTTLCD LADRELVVII GWAKHIPGFS TSLADQMSL  
301 LQSAWMEILI LGVVYRSLSF EDELVYADDY IMDEDQSKLA GLLDLNNAIL  
351 QLVKKYKSMK LEKEEFVTLK AIALANSDSM HIEDVEAVQK LQDVLHEALQ  
401 DYEAGQHMED PRRAGKMLMT LPLLEQTSTK AVQHFYNIKL EGKVPMHKLF  
451 LEMLEAKV\* (SEQ ID NO:4)

FIG. 6

1 GCGGGCCGCC AGTGTGGTGG AATTCGGCTT GTCACTAGGA GAACATTTGT  
51 GTTAATTGCA CTGTGCTCTG TCAAGGAAAC TTTGATTTAT AGCTGGGGTG  
101 CACAAATAAT GGTGCGCGT CGCACATGGA TTCGGTAGAA CTTTGCCTTC  
151 CTGAATCTTT TTCCCTGCAC TACGAGGAAG AGCTTCTCTG CAGAATGTCA  
201 AACAAAGATC GACACATTGA TTCCAGCTGT TCGTCCTTCA TCAAGACGGA  
251 ACCTTCCAGC CCAGCCTCCC TGACGGACAG CGTCAACCAC CACAGCCCTG  
301 GTGGCTCTTC AGACGCCAGT GGGAGCTACA GTTCAACCAT GAATGGCCAT  
351 CAGAACGGAC TTGACTCGCC ACCTCTCTAC CTTTCTGCTC CTATCCTGGG  
401 AGGTAGTGGG CCTGTCAGGA AACTGTATGA TGA CTGCTCC AGCACCATTG  
451 TTGAAGATCC CCAGACCAAG TGTGAATACA TGCTCAACTC GATGCCCAAG  
501 AGACTGTGTT TAGTGTGTGG TGACATCGCT TCTGGGTACC ACTATGGGGT  
551 AGCATCATGT GAAGCCTGCA AGGCATTCTT CAAGAGGACA ATTCAAGGCA  
601 ATATAGAATA CAGCTGCCCT GCCACGAATG AATGTGAAAT CACAAAGCGC  
651 AGACGTAAAT CCTGCCAGGC TTGCCGCTTC ATGAAGTGTT TAAAAGTGGG  
701 CATGCTGAAA GAAGGGGTGC GTCTTGACAG AGTACGTGGA GGTGCGCAGA  
751 AGTACAAGCG CAGGATAGAT GCGGAGAACA GCCCATACCT GAACCCTCAG  
801 CTGGTTCAGC CAGCCAAAAA GCCATATAAC AAGATTGTCT CACATTTGTT  
851 GGTGGCTGAA CCGGAGAAGA TCTATGCCAT GCCTGACCCT ACTGTCCCCG  
901 ACAGTGACAT CAAAGCCCTC ACTACACTGT GTGACTTGGC CGACCGAGAG  
951 TTGGTGGTTA TCATTGGATG GGCGAAGCAT ATTCCAGGCT TCTCCACGCT  
1001 GTCCCTGGCG GACCAGATGA GCCTTCTGCA GAGTGCTTGG ATGGAAATTT

FIG.7A

1051 TGATCCTTGG TGTCGTATAC CGGTCTCTTT CATTTGAGGA TGAACCTGTC  
1101 TATGCAGACG ATTATATAAT GGACGAAGAC CAGTCCAAAT TAGCAGGCCT  
1151 TCTTGATCTA AATAATGCTA TCCTGCAGCT GGTAAGAAA TACAAGAGCA  
1201 TGAAGCTGGA AAAAGAAGAA TTTGTCACCC TCAAAGCTAT AGCTCTTGCT  
1251 AATTCAGACT CCATGCACAT AGAAGATGTT GAAGCCGTTT AGAAGCTTCA  
1301 GGATGTCTTA CATGAAGCGC TGCAGGATTA TGAAGCTGGC CAGCACATGG  
1351 AGAAGACCCT CGTCGAGCTG GCAAGATGCT GATGACACTG CCACTCCTGA  
1401 GGCAGACCTC TACCAAGGCC GTGCAGCATT TCTACAACAT CAACTAGAA  
1451 GGCAAAGTCC CAATGCACAA ACTTTTTTTG GAAATGTTGG AGGCCAAGGT  
1501 CTGACTAAAA GCTCCCTGGG CCTTCCCATC CTTTCATGTTG AAAAAGGGAA  
1551 AATAAACCCA AGAGTGATGT CGAAGAACT TAGAGTTTAG TTAACAACAT  
1601 CAAAAATCAA CAGACTGCAC TGATAATTTA GCAGCAAGAC TATGAAGCAG  
1651 CTTTCAGATT CCTCCATAGG TTCCTGATGA GTTCTTTCTA CTTTCTCCAT  
1701 CATCTTCTTT CCTCTTTCTT CCCACATTTT TCTTTCTCTT TATTTTTTCT  
1751 CCTTTTCTTC TTTCACCTCC CTTATTTCTT TGCTTCTTTC ATTCCTAGTT  
1801 CCCATTCTCC TTTATTTTCT TCCCGTCTGC CTGCCTTCTT TCTTTTCTTT  
1851 ACCTACTCTC ATTCCTCTCT TTTCTCATCC TTCCCTTTT TTCTAAATTT  
1901 GAAATAGCTT TAGTTTAAAA AAAAAATCC TCCCTTCCCC CTTTCCTTTC  
1951 CCTTTCTTTC CTTTTTCCCT TTCCTTTTCC CTTTCCTTTC CTTTCCTCTT  
2001 GACCTTCTTT CCATCTTTCT TTTTCTTCCT TCTGCTGCTG AACTTTTAAA  
2051 AGAGGTCTCT AACTGAAGAG AGATGGAAGC CAGCCCTGCC AAAGGATGGA

FIG.7B



2101 GATCCATAAT ATGGATGCCA GTGAACTTAT TGTGAACCAT ACCGTCCCCA  
2151 ATGACTAAGG AATCAAAGAG AGAGAACCAA CGTTCCTAAA AGTACAGTGC  
2201 AACATATACA AATTGACTGA GTGCAGTATT AGATTTTCATG GGAGCAGCCT  
2251 CTAATTAGAC AACTTAAGCA ACGTTGCATC GGCTGCTTCT TATCATTGCT  
2301 TTTCCATCTA GATCAGTTAC AGCCATTTGA TTCCTTAATT GTTTTTTCAA  
2351 GTCTTCCAGG TATTTGTTAG TTTAGCTACT ATGTAACTTT TTCAGGGAAT  
2401 AGTTTAAGCT TTATTCATTC ATGCAATACT AAAGAGAAAT AAGAATACTG  
2451 CAATTTTGTG CTGGCTTTGA ACAATTACGA ACAATAATGA AGGACAAATG  
2501 AATCCTGAAG GAAGATTTTT AAAAATGTTT TGTTTCTTCT TACAAATGGA  
2551 GATTTTTTTG TACCAGCTTT ACCACTTTTC AGCCATTTAT TAATATGGGA  
2601 ATTTAACTTA CTCAAGCAAT AGTTGAAGGG AAGGTGCATA TTATCACGGA  
2651 TGCAATTTAT GTTGTGTGCC AGTCTGGTCC CAAACATCAA TTTCTTAACA  
2701 TGAGCTCCAG TTTACCTAAA TGTTCACTGA CACAAAGGAT GAGATTACAC  
2751 CTACAGTGAC TCTGAGTAGT CACATATATA AGCACTGCAC ATGAGATATA  
2801 GATCCGTAGA ATTGTCAGGA GTGCACCTCT GTACTTGGGA GGTACAATTG  
2851 CCATATGATT TCTAGCTGCC ATGGTGGTTA GGAATGTGAT ACTGCCTGTT  
2901 TGCAAAGTCA CAGACCTTGC CTCAGAAGGA GCTGTGAGCC AGTATTCATT  
2951 TAAGAGAATT CCACCACACT GGCGGCCCGC GCTTGAT (SEQ ID NO:5)

FIG.7C

1 MDSVELCLPE SFSLHYEEL LCRMSNKDRH IDSSCSSFIK TEPSSPASLT  
51 DSVNHHSPGG SSDASGSYSS TMNGHQGLD SPPLYPAPI LGGSGPVRKL  
101 TDDCSSTIVE DPQTKCEYML NSMPKRL CLV CGDIASGYHY GVASCEACKA  
151 FFKRTIOGNI IYSCPATNEC EITKRRRKSC OACRFMKCLK VGMLKEGVRL  
201 DRVRGGGRQKY KRRIDAENSP YLNPQLVQPA KKPYNKIVSH LLVAEPEKIY  
251 AMPDPTVPDS DIKALTTLCD LADRELVVII GWAKHIPGFS TSLADQMSL  
301 LQSAWMEILI LGVVYRSLSF EDELVYADDY IMDEDQSKLA GLLDLNNAIL  
351 QLVKKYKSMK LEKEEFVTLK AIALANSDSM HIEDVEAVQK LQDVLHEALQ  
401 DYEAGQHMEK TLVELARC\* (SEQ ID NO:6)

FIG.8